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ARAND et al

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SEQUENCE LISTING

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#8

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 ARCHELAS, ALAIN ROBERT
 BARATI, JACQUES
 FURSTOSS, ROLAND

<120> EPOXIDE HYDROLASES OF ASPERGILLUS ORIGIN

<130> bml-410.018

<140> 10/009,030

<141> 2001-11-02

<150> PCT/FR00/01217

<151> 2000-05-05

<150> FR 99/05711

<151> 1999-05-05

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 1197

<212> DNA

<213> Aspergillus niger

<220>

<221> CDS

<222> (1)..(1194)

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Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys	
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acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg	144
Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu	
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caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg	192
Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met	
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cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga	240
Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg	
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ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att	288
Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile	
85 90 95	

cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca	336
His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala	
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ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg	384
Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu	
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Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu	
130 135 140	
gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg	480
Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu	
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Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu	
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Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp	
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att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc	624
Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys	
195 200 205	
aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc	672
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Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro	
275 280 285	
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305 310 315 320	

gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att 1008
 Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
 325 330 335

cac aag ccg ttt ggg ttc tcc ttc ttc ccc aag gac ctt tgt cct gtg 1056
 His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val
 340 345 350

cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat 1104
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 355 360 365

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<213> Aspergillus niger

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 35 40 45

Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
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Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
 65 70 75 80

Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
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His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
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Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
 115 120 125

Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
 130 135 140

Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu
 145 150 155 160

Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu
 165 170 175
 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp
 180 185 190
 Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
 195 200 205
 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
 210 215 220
 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg
 225 230 235 240
 Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser
 245 250 255
 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala
 260 265 270
 Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro
 275 280 285
 Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr
 290 295 300
 Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr
 305 310 315 320
 Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
 325 330 335
 His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val
 340 345 350
 Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<212> DNA
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<223> Description of Artificial Sequence: Primer

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44

SEQUENCE LISTING

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 PROCESSES FOR OBTAINING THEM, AND THEIR USES, IN
 PARTICULAR FOR THE PREPARATION OF ENANTIOMERICALLY
 PURE MOLECULES

10 <130> EPOXSL

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15 <160> 2

<170> PatentIn Ver. 2.1

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20 <211> 1197

<212> DNA

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25 <221> CDS

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 Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys
 20 25 30

40 acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144
 Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
 35 40 45

45 caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg 192
 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
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cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga 240
 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
 65 70 75 80

50 ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att 288
 Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
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55 cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca 336
 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
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60 ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg 384
 Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
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	130 135 140	
5	gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg	480
	Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu	
	145 150 155 160	
10	gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg	528
	Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu	
	165 170 175	
15	atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat	576
	Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp	
	180 185 190	
20	att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc	624
	Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys	
	195 200 205	
25	aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag gcc	672
	Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly	
	210 215 220	
30	ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga	720
	Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg	
	225 230 235 240	
35	atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt	768
	Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser	
	245 250 255	
40	act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca	816
	Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala	
	260 265 270	
45	tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc	864
	Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro	
	275 280 285	
50	ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg	912
	Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr	
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55	gaa agt ttc ccg cgg gca att cat acc tac cgc gag act acc cca act	960
	Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr	
	305 310 315 320	
60	gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att	1008
	Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile	
	325 330 335	
65	cac aag ccg ttt ggg ttc tcc ttc ttc ccc aag gac ctt tgt cct gtg	1056
	His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val	
	340 345 350	
70	cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat	1104
	Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp	
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cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg 1152
 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu
 370 375 380

5 aag acc gac ctg aca gca ttt gtc gag cag gtg tgg cag aag tag 1197
 Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys
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25 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
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30 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
 65 70 75 80

Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
 85 90 95

35 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
 100 105 110

Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
 115 120 125

40 Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
 130 135 140

45 Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu
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Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu
 165 170 175

50 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp
 180 185 190

Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
 195 200 205

55 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
 210 215 220

60 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg
 225 230 235 240

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				260					265					270			
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